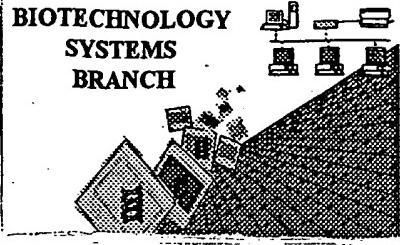


*Anne
Baker*

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/508,828A
Source: 1600 RUSH
Date Processed by STIC: 3/13/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** **SERIAL NUMBER:** 09/508,828A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleic
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
- 2 Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length

Sequence(s) 10 contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (ii) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/508,828A

DATE: 03/13/2002
TIME: 10:49:53

Input Set : A:\SCH-32409.txt
Output Set: N:\CRF3\03132002\I508828A.raw

3 <110> APPLICANT: Prionics AG
4 Moser, Markus
5 Oesch, Bruno
6 Korth, Carsten
8 <120> TITLE OF INVENTION: SYNTHETIC POLYPEPTIDE FOR DIAGNOSING AND TREATING PRION-
RELATED DISEASES
10 <130> FILE REFERENCE: SCH-32409
12 <140> CURRENT APPLICATION NUMBER: 09/508,828A
~~OK~~ 13 <141> CURRENT FILING DATE: 2000-07-27
15 <150> PRIOR APPLICATION NUMBER: PCT/EP98/05924
16 <151> PRIOR FILING DATE: 1998-09-17
18 <160> NUMBER OF SEQ ID NOS: 12
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 9
24 <212> TYPE: PRT
25 <213> ORGANISM: Bos taurus
27 <220> FEATURE:
28 <221> NAME/KEY: misc_feature
29 <222> LOCATION: (2)..(2)
30 <223> OTHER INFORMATION: Asn or Ser
33 <220> FEATURE:
34 <221> NAME/KEY: misc_feature
35 <222> LOCATION: (4)..(4)
36 <223> OTHER INFORMATION: Trp or Tyr
39 <220> FEATURE:
40 <221> NAME/KEY: misc_feature
41 <222> LOCATION: (8)..(9)
42 <223> OTHER INFORMATION: The Tyr-Tyr at positions 8-9 may be absent
45 <400> SEQUENCE: 1
~~W~~ 47 Gly Xaa Asp Xaa Glu Asp Arg Tyr Tyr
48 1 5
51 <210> SEQ ID NO: 2
52 <211> LENGTH: 13
53 <212> TYPE: PRT
54 <213> ORGANISM: Bos taurus
56 <220> FEATURE:
57 <221> NAME/KEY: misc_feature
58 <222> LOCATION: (5)..(5)
59 <223> OTHER INFORMATION: Arg or Lys
62 <220> FEATURE:
63 <221> NAME/KEY: misc_feature
64 <222> LOCATION: (7)..(7)
65 <223> OTHER INFORMATION: Met ^{or} Val or Ala

pp. 51
Does Not Comply
Corrected Diskette Needed
please edit

Input Set : A:\SCH-32409.txt
Output Set: N:\CRF3\03132002\I508828A.raw

68 <220> FEATURE:
69 <221> NAME/KEY: misc_feature
70 <222> LOCATION: (9)..(9) /
71 <223> OTHER INFORMATION: Gln or Glu or Arg
74 <220> FEATURE:
75 <221> NAME/KEY: misc_feature
76 <222> LOCATION: (11)..(11) /
77 <223> OTHER INFORMATION: Ser or Asn
80 <220> FEATURE:
81 <221> NAME/KEY: misc_feature
82 <222> LOCATION: (1)..(1)
83 <223> OTHER INFORMATION: The Gln at position 1 may be absent
86 <220> FEATURE:
87 <221> NAME/KEY: misc_feature
88 <222> LOCATION: (2)..(2)
89 <223> OTHER INFORMATION: The Val at position 2 may be absent
92 <220> FEATURE:
93 <221> NAME/KEY: misc_feature
94 <222> LOCATION: (12)..(13)
95 <223> OTHER INFORMATION: The Asn-Gln at position 12-13 may be absent
98 <400> SEQUENCE: 2 / /
WK> 100 Gln Val Tyr Tyr Xaa Pro Xaa Asp Xaa Tyr Xaa Asn Gln
101 1 5 10
104 <210> SEQ ID NO: 3
105 <211> LENGTH: 13
106 <212> TYPE: PRT
107 <213> ORGANISM: Bos taurus
109 <220> FEATURE:
110 <221> NAME/KEY: misc_feature /
111 <222> LOCATION: (2)..(2)
112 <223> OTHER INFORMATION: Val or Thr or Ile
115 <220> FEATURE:
116 <221> NAME/KEY: misc_feature /
117 <222> LOCATION: (6)..(6)
118 <223> OTHER INFORMATION: Gln or Glu
121 <220> FEATURE:
122 <221> NAME/KEY: misc_feature /
123 <222> LOCATION: (7)..(7)
124 <223> OTHER INFORMATION: Lys or Arg or Gln
127 <220> FEATURE:
128 <221> NAME/KEY: misc_feature /
129 <222> LOCATION: (10)..(10)
130 <223> OTHER INFORMATION: Gln or Glu
133 <220> FEATURE:
134 <221> NAME/KEY: misc_feature /
135 <222> LOCATION: (12)..(12)
136 <223> OTHER INFORMATION: Tyr or Ser or Ala
139 <220> FEATURE:
140 <221> NAME/KEY: misc_feature

Input Set : A:\SCH-32409.txt
Output Set: N:\CRF3\03132002\I508828A.raw

141 <222> LOCATION: (12)..(13)
142 <223> OTHER INFORMATION: The Xaa and Tyr at positions 12-13 may be absent
145 <400> SEQUENCE: 3 / / /
W-> 147 Cys Xaa Thr Gln Tyr Xaa Xaa Glu Ser Xaa Ala Xaa Tyr
148 1 5 10
151 <210> SEQ ID NO: 4
152 <211> LENGTH: 13
153 <212> TYPE: PRT
154 <213> ORGANISM: Bos taurus
156 <220> FEATURE:
157 <221> NAME/KEY: misc_feature
158 <222> LOCATION: (6)..(6)
159 <223> OTHER INFORMATION: His or Tyr or Asn
162 <220> FEATURE:
163 <221> NAME/KEY: misc_feature
164 <222> LOCATION: (1)..(2)
165 <223> OTHER INFORMATION: The Tyr-Arg at positions 1-2 may be absent
168 <220> FEATURE:
169 <221> NAME/KEY: misc_feature
170 <222> LOCATION: (11)..(13) /
171 <223> OTHER INFORMATION: The Gln-Val-Tyr at positions 11-13 may be absent
174 <400> SEQUENCE: 4 /
Q-> 176 Tyr Arg Glu Asn Met Xaa Arg Tyr Pro Asn Gln Val Tyr
177 1 5 10
180 <210> SEQ ID NO: 5
181 <211> LENGTH: 15
182 <212> TYPE: PRT
183 <213> ORGANISM: Bos taurus
185 <400> SEQUENCE: 5
187 Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro His Gly
188 1 5 10 15
191 <210> SEQ ID NO: 6
192 <211> LENGTH: 14
193 <212> TYPE: PRT
194 <213> ORGANISM: Bos taurus
196 <220> FEATURE:
197 <221> NAME/KEY: misc_feature
198 <222> LOCATION: (3)..(3) /
199 <223> OTHER INFORMATION: Asn or Ser
202 <220> FEATURE:
203 <221> NAME/KEY: misc_feature
204 <222> LOCATION: (8)..(8) /
205 <223> OTHER INFORMATION: Asn or Ser
208 <220> FEATURE:
209 <221> NAME/KEY: misc_feature /
210 <222> LOCATION: (9)..(9) /
211 <223> OTHER INFORMATION: Met or Leu or Phe
214 <220> FEATURE:
215 <221> NAME/KEY: misc_feature

Input Set : A:\SCH-32409.txt
Output Set: N:\CRF3\03132002\I508828A.raw

216 <222> LOCATION: (12)..(12)
217 <223> OTHER INFORMATION: Met or Val
220 <400> SEQUENCE: 6
W- 222 Lys Pro Xaa Lys Pro Lys Thr Xaa Xaa Lys His Xaa Ala Gly
223 1 5 10
226 <210> SEQ ID NO: 7
227 <211> LENGTH: 5
228 <212> TYPE: PRT
229 <213> ORGANISM: Bos taurus
231 <220> FEATURE:
232 <221> NAME/KEY: misc_feature
233 <222> LOCATION: (2)..(2)
234 <223> OTHER INFORMATION: Met or Val
237 <400> SEQUENCE: 7
W- 239 Tyr Xaa Leu Gly Ser
240 1 5
243 <210> SEQ ID NO: 8
244 <211> LENGTH: 13
245 <212> TYPE: PRT
246 <213> ORGANISM: Bos taurus
248 <220> FEATURE:
249 <221> NAME/KEY: misc_feature
250 <222> LOCATION: (7)..(7)
251 <223> OTHER INFORMATION: Ile or Leu or Met
254 <220> FEATURE:
255 <221> NAME/KEY: misc_feature
256 <222> LOCATION: (8)..(8)
257 <223> OTHER INFORMATION: Ile or Leu or Met
260 <220> FEATURE:
261 <221> NAME/KEY: misc_feature
262 <222> LOCATION: (12)..(12)
263 <223> OTHER INFORMATION: Asn or Ser
266 <400> SEQUENCE: 8
W- 268 Ser Ala Met Ser Arg Pro Xaa Xaa His Phe Gly Xaa Asp
269 1 5 10
272 <210> SEQ ID NO: 9
273 <211> LENGTH: 12
274 <212> TYPE: PRT
275 <213> ORGANISM: Bos taurus
277 <220> FEATURE:
278 <221> NAME/KEY: misc_feature
279 <222> LOCATION: (3)..(3)
280 <223> OTHER INFORMATION: His or Tyr or Asn
283 <220> FEATURE:
284 <221> NAME/KEY: misc_feature
285 <222> LOCATION: (7)..(7)
286 <223> OTHER INFORMATION: Asn or Ser
289 <220> FEATURE:
290 <221> NAME/KEY: misc_feature

Input Set : A:\SCH-32409.txt
Output Set: N:\CRF3\03132002\I508828A.raw

291 <222> LOCATION: (12)..(12)
292 <223> OTHER INFORMATION: Lys or Arg
295 <220> FEATURE:
296 <221> NAME/KEY: misc_feature
297 <222> LOCATION: (6)..(7)
298 <223> OTHER INFORMATION: The Pro-Xaa at positions 6-7 may be absent
301 <220> FEATURE:
302 <221> NAME/KEY: misc_feature
303 <222> LOCATION: (8)..(12)
304 <223> OTHER INFORMATION: The Gln-Val-Tyr-Tyr-Xaa at positions 8-12 may be absent
307 <400> SEQUENCE: 9
QV> 309 Asn Met Xaa Arg Tyr Pro Xaa Gln Val Tyr Tyr Xaa
310 1 5 10
313 <210> SEQ ID NO: 10
314 <211> LENGTH: 23
315 <212> TYPE: PRT
316 <213> ORGANISM: Bos taurus
318 <220> FEATURE:
319 <221> NAME/KEY: misc_feature
320 <222> LOCATION: (11)..(11)
321 <223> OTHER INFORMATION: Met or Val
324 <220> FEATURE:
325 <221> NAME/KEY: misc_feature *Xaa can only represent a single amino acid.*
326 <222> LOCATION: (12)..(12) *see item 5*
327 <223> OTHER INFORMATION: *This is a conventional spacer, for instance Gly-Gly*
330 <220> FEATURE:
331 <221> NAME/KEY: misc_feature
332 <222> LOCATION: (15)..(15)
333 <223> OTHER INFORMATION: Arg or Lys
336 <220> FEATURE:
337 <221> NAME/KEY: misc_feature
338 <222> LOCATION: (17)..(17)
339 <223> OTHER INFORMATION: Met or Val or Ala
342 <220> FEATURE:
343 <221> NAME/KEY: misc_feature
344 <222> LOCATION: (19)..(19)
345 <223> OTHER INFORMATION: Gln or Glu or Arg
348 <220> FEATURE:
349 <221> NAME/KEY: misc_feature
350 <222> LOCATION: (21)..(21)
351 <223> OTHER INFORMATION: Ser or Asn
354 <220> FEATURE:
355 <221> NAME/KEY: misc_feature
356 <222> LOCATION: (1)..(1)
357 <223> OTHER INFORMATION: The Gly at position 1 may be absent
360 <220> FEATURE:
361 <221> NAME/KEY: misc_feature
362 <222> LOCATION: (11)..(11)
363 <223> OTHER INFORMATION: The Xaa at position 11 may be absent

*Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/508,828A

DATE: 03/13/2002

TIME: 10:49:54

Input Set : A:\SCH-32409.txt

Output Set: N:\CRF3\03132002\I508828A.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:47 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:176 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:239 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:443 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11